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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/488,265

DATE: 07/19/2001

TIME: 16:47:33

Input Set : A:\5808.200-US(sequence).ST25.txt

Output Set: N:\CRF3\07192001\I488265.raw

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3 <110> APPLICANT: Lehmann, Martin
4 Lassen, Soren F
6 <120> TITLE OF INVENTION: Improved Phytases
8 <130> FILE REFERENCE: 5808.200-US
10 <140> CURRENT APPLICATION NUMBER: 09/488265
11 <141> CURRENT FILING DATE: 2000-01-20
13 <160> NUMBER OF SEQ ID NOS: 98
15 <170> SOFTWARE: PatentIn version 3.1
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 440
19 <212> TYPE: PRT
20 <213> ORGANISM: Aspergillus terreus 9A-1
22 <400> SEQUENCE: 1
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25 1 5 10 15
28 Glu Leu Ser His Lys Trp Gly Leu Tyr Ala Pro Tyr Phe Ser Leu Gln
29 20 25 30
32 Asp Glu Ser Pro Phe Pro Leu Asp Val Pro Glu Asp Cys His Ile Thr
33 35 40 45
36 Phe Val Gln Val Leu Ala Arg His Gly Ala Arg Ser Pro Thr His Ser
37 50 55 60
40 Lys Thr Lys Ala Tyr Ala Ala Thr Ile Ala Ala Ile Gln Lys Ser Ala
41 65 70 75 80
44 Thr Ala Phe Pro Gly Lys Tyr Ala Phe Leu Gln Ser Tyr Asn Tyr Ser
45 85 90 95
48 Leu Asp Ser Glu Glu Leu Thr Pro Phe Gly Arg Asn Gln Leu Arg Asp
49 100 105 110
52 Leu Gly Ala Gln Phe Tyr Glu Arg Tyr Asn Ala Leu Thr Arg His Ile
53 115 120 125
56 Asn Pro Phe Val Arg Ala Thr Asp Ala Ser Arg Val His Glu Ser Ala
57 130 135 140
60 Glu Lys Phe Val Glu Gly Phe Gln Thr Ala Arg Gln Asp Asp His His
61 145 150 155 160
64 Ala Asn Pro His Gln Pro Ser Pro Arg Val Asp Val Ala Ile Pro Glu
65 165 170 175
68 Gly Ser Ala Tyr Asn Asn Thr Leu Glu His Ser Leu Cys Thr Ala Phe
69 180 185 190
72 Glu Ser Ser Thr Val Gly Asp Asp Ala Val Ala Asn Phe Thr Ala Val
73 195 200 205
76 Phe Ala Pro Ala Ile Ala Gln Arg Leu Glu Ala Asp Leu Pro Gly Val
77 210 215 220
80 Gln Leu Ser Thr Asp Asp Val Val Asn Leu Met Ala Met Cys Pro Phe
81 225 230 235 240
84 Glu Thr Val Ser Leu Thr Asp Asp Ala His Thr Leu Ser Pro Phe Cys
85 245 250 255
88 Asp Leu Phe Thr Ala Thr Glu Trp Thr Gln Tyr Asn Tyr Leu Leu Ser
89 260 265 270

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92 Leu Asp Lys Tyr Tyr Gly Tyr Gly Gly Asn Pro Leu Gly Pro Val
 93 275 280 285
 96 Gln Gly Val Gly Trp Ala Asn Glu Leu Met Ala Arg Leu Thr Arg Ala
 97 290 295 300
 100 Pro Val His Asp His Thr Cys Val Asn Asn Thr Leu Asp Ala Ser Pro
 101 305 310 315 320
 104 Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp
 105 325 330 335
 108 Ser Asn Leu Val Ser Ile Phe Trp Ala Leu Gly Leu Tyr Asn Gly Thr
 109 340 345 350
 112 Ala Pro Leu Ser Gln Thr Ser Val Glu Ser Val Ser Gln Thr Asp Gly
 113 355 360 365
 116 Tyr Ala Ala Ala Trp Thr Val Pro Phe Ala Ala Arg Ala Tyr Val Glu
 117 370 375 380
 120 Met Met Gln Cys Arg Ala Glu Lys Glu Pro Leu Val Arg Val Leu Val
 121 385 390 395 400
 124 Asn Asp Arg Val Met Pro Leu His Gly Cys Pro Thr Asp Lys Leu Gly
 125 405 410 415
 128 Arg Cys Lys Arg Asp Ala Phe Val Ala Gly Leu Ser Phe Ala Gln Ala
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 137 <211> LENGTH: 440
 138 <212> TYPE: PRT
 139 <213> ORGANISM: Aspergillus terreus cbs
 141 <400> SEQUENCE: 2
 143 Asn His Ser Asp Cys Thr Ser Val Asp Arg Gly Tyr Gln Cys Phe Pro
 144 1 5 10 15
 147 Glu Leu Ser His Lys Trp Gly Leu Tyr Ala Pro Tyr Phe Ser Leu Gln
 148 20 25 30
 151 Asp Glu Ser Pro Phe Pro Leu Asp Val Pro Asp Asp Cys His Ile Thr
 152 35 40 45
 155 Phe Val Gln Val Leu Ala Arg His Gly Ala Arg Ser Pro Thr Asp Ser
 156 50 55 60
 159 Lys Thr Lys Ala Tyr Ala Ala Thr Ile Ala Ala Ile Gln Lys Asn Ala
 160 65 70 75 80
 163 Thr Ala Leu Pro Gly Lys Tyr Ala Phe Leu Lys Ser Tyr Asn Tyr Ser
 164 85 90 95
 167 Met Gly Ser Glu Asn Leu Thr Pro Phe Gly Arg Asn Gln Leu Gln Asp
 168 100 105 110
 171 Leu Gly Ala Gln Phe Tyr Arg Arg Tyr Asp Thr Leu Thr Arg His Ile
 172 115 120 125
 175 Asn Pro Phe Val Arg Ala Ala Asp Ser Ser Arg Val His Glu Ser Ala
 176 130 135 140
 179 Glu Lys Phe Val Glu Gly Phe Gln Asn Ala Arg Gln Gly Asp Pro His
 180 145 150 155 160
 183 Ala Asn Pro His Gln Pro Ser Pro Arg Val Asp Val Val Ile Pro Glu
 184 165 170 175

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187 Gly Thr Ala Tyr Asn Asn Thr Leu Glu His Ser Ile Cys Thr Ala Phe
188 180 185 190
191 Glu Ala Ser Thr Val Gly Asp Ala Ala Ala Asp Asn Phe Thr Ala Val
192 195 200 205
195 Phe Ala Pro Ala Ile Ala Lys Arg Leu Glu Ala Asp Leu Pro Gly Val
196 210 215 220
199 Gln Leu Ser Ala Asp Asp Val Val Asn Leu Met Ala Met Cys Pro Phe
200 225 230 235 240
203 Glu Thr Val Ser Leu Thr Asp Asp Ala His Thr Leu Ser Pro Phe Cys
204 245 250 255
207 Asp Leu Phe Thr Ala Ala Glu Trp Thr Gln Tyr Asn Tyr Leu Leu Ser
208 260 265 270
211 Leu Asp Lys Tyr Tyr Gly Tyr Gly Gly Asn Pro Leu Gly Pro Val
212 275 280 285
215 Gln Gly Val Gly Trp Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser
216 290 295 300
219 Pro Val His Asp His Thr Cys Val Asn Asn Thr Leu Asp Ala Asn Pro
220 305 310 315 320
223 Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp
224 325 330 335
227 Ser Asn Leu Val Ser Ile Phe Trp Ala Leu Gly Leu Tyr Asn Gly Thr
228 340 345 350
231 Lys Pro Leu Ser Gln Thr Thr Val Glu Asp Ile Thr Arg Thr Asp Gly
232 355 360 365
235 Tyr Ala Ala Ala Trp Thr Val Pro Phe Ala Ala Arg Ala Tyr Ile Glu
236 370 375 380
239 Met Met Gln Cys Arg Ala Glu Lys Gln Pro Leu Val Arg Val Leu Val
240 385 390 395 400
243 Asn Asp Arg Val Met Pro Leu His Gly Cys Ala Val Asp Asn Leu Gly
244 405 410 415
247 Arg Cys Lys Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ala
248 420 425 430
251 Gly Gly Asn Trp Ala Glu Cys Phe
252 435 440
255 <210> SEQ ID NO: 3
256 <211> LENGTH: 441
257 <212> TYPE: PRT
258 <213> ORGANISM: Asergillus niger var. awamori
260 <400> SEQUENCE: 3
262 Asn Gln Ser Thr Cys Asp Thr Val Asp Gln Gly Tyr Gln Cys Phe Ser
263 1 5 10 15
266 Glu Thr Ser His Leu Trp Gly Gln Tyr Ala Pro Phe Phe Ser Leu Ala
267 20 25 30
270 Asn Glu Ser Ala Ile Ser Pro Asp Val Pro Ala Gly Cys Arg Val Thr
271 35 40 45
274 Phe Ala Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Glu Ser
275 50 55 60
278 Lys Gly Lys Lys Tyr Ser Ala Leu Ile Glu Glu Ile Gln Gln Asn Val
279 65 70 75 80

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282 Thr Thr Phe Asp Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Ser
283 85 90 95
286 Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Glu Leu Val Asn
287 100 105 110
290 Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Glu Ser Leu Thr Arg Asn Ile
291 115 120 125
294 Ile Pro Phe Ile Arg Ser Ser Gly Ser Ser Arg Val Ile Ala Ser Gly
295 130 135 140
298 Glu Lys Phe Ile Glu Gly Phe Gln Ser Thr Lys Leu Lys Asp Pro Arg
299 145 150 155 160
302 Ala Gln Pro Gly Gln Ser Ser Pro Lys Ile Asp Val Val Ile Ser Glu
303 165 170 175
306 Ala Ser Ser Ser Asn Asn Thr Leu Asp Pro Gly Thr Cys Thr Val Phe
307 180 185 190
310 Glu Asp Ser Glu Leu Ala Asp Thr Val Glu Ala Asn Phe Thr Ala Thr
311 195 200 205
314 Phe Ala Pro Ser Ile Arg Gln Arg Leu Glu Asn Asp Leu Ser Gly Val
315 210 215 220
318 Thr Leu Thr Asp Thr Glu Val Thr Tyr Leu Met Asp Met Cys Ser Phe
319 225 230 235 240
322 Asp Thr Ile Ser Thr Ser Thr Val Asp Thr Lys Leu Ser Pro Phe Cys
323 245 250 255
326 Asp Leu Phe Thr His Asp Glu Trp Ile His Tyr Asp Tyr Leu Gln Ser
327 260 265 270
330 Leu Lys Lys Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu Gly Pro Thr
331 275 280 285
334 Gln Gly Val Gly Tyr Ala Asn Glu Leu Ile Ala Arg Leu Thr His Ser
335 290 295 300
338 Pro Val His Asp Asp Thr Ser Ser Asn His Thr Leu Asp Ser Asn Pro
339 305 310 315 320
342 Ala Thr Phe Pro Leu Asn Ser Thr Leu Tyr Ala Asp Phe Ser His Asp
343 325 330 335
346 Asn Gly Ile Ile Ser Ile Leu Phe Ala Leu Gly Leu Tyr Asn Gly Thr
347 340 345 350
350 Lys Pro Leu Ser Thr Thr Val Glu Asn Ile Thr Gln Thr Asp Gly
351 355 360 365
354 Phe Ser Ser Ala Trp Thr Val Pro Phe Ala Ser Arg Leu Tyr Val Glu
355 370 375 380
358 Met Met Gln Cys Gln Ala Glu Gln Glu Pro Leu Val Arg Val Leu Val
359 385 390 395 400
362 Asn Asp Arg Val Val Pro Leu His Gly Cys Pro Ile Asp Ala Leu Gly
363 405 410 415
366 Arg Cys Thr Arg Asp Ser Phe Val Arg Gly Leu Ser Phe Ala Arg Ser
367 420 425 430
370 Gly Gly Asp Trp Ala Glu Cys Ser Ala
371 435 440
374 <210> SEQ ID NO: 4
375 <211> LENGTH: 441
376 <212> TYPE: PRT

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Input Set : A:\5808.200-US(sequence).ST25.txt
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377 <213> ORGANISM: Aspergillus niger T213
 379 <400> SEQUENCE: 4
 381 Asn Gln Ser Ser Cys Asp Thr Val Asp Gln Gly Tyr Gln Cys Phe Ser
 382 1 5 10 15
 385 Glu Thr Ser His Leu Trp Gly Gln Tyr Ala Pro Phe Phe Ser Leu Ala
 386 20 25 30
 389 Asn Glu Ser Val Ile Ser Pro Asp Val Pro Ala Gly Cys Arg Val Thr
 390 35 40 45
 393 Phe Ala Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr Glu Ser
 394 50 55 60
 397 Lys Gly Lys Lys Tyr Ser Ala Leu Ile Glu Glu Ile Gln Gln Asn Val
 398 65 70 75 80
 401 Thr Thr Phe Asp Gly Lys Tyr Ala Phe Leu Lys Thr Tyr Asn Tyr Ser
 402 85 90 95
 405 Leu Gly Ala Asp Asp Leu Thr Pro Phe Gly Glu Gln Glu Leu Val Asn
 406 100 105 110
 409 Ser Gly Ile Lys Phe Tyr Gln Arg Tyr Glu Ser Leu Thr Arg Asn Ile
 410 115 120 125
 413 Ile Pro Phe Ile Arg Ser Ser Gly Ser Ser Arg Val Ile Ala Ser Gly
 414 130 135 140
 417 Glu Lys Phe Ile Glu Gly Phe Gln Ser Thr Lys Leu Lys Asp Pro Arg
 418 145 150 155 160
 421 Ala Gln Pro Gly Gln Ser Ser Pro Lys Ile Asp Val Val Ile Ser Glu
 422 165 170 175
 425 Ala Ser Ser Ser Asn Asn Thr Leu Asp Pro Gly Thr Cys Thr Val Phe
 426 180 185 190
 429 Glu Asp Ser Glu Leu Ala Asp Thr Val Glu Ala Asn Phe Thr Ala Thr
 430 195 200 205
 433 Phe Ala Pro Ser Ile Arg Gln Arg Leu Glu Asn Asp Leu Ser Gly Val
 434 210 215 220
 437 Thr Leu Thr Asp Thr Glu Val Thr Tyr Leu Met Asp Met Cys Ser Phe
 438 225 230 235 240
 441 Asp Thr Ile Ser Thr Ser Thr Val Asp Thr Lys Leu Ser Pro Phe Cys
 442 245 250 255
 445 Asp Leu Phe Thr His Asp Glu Trp Ile His Tyr Asp Tyr Leu Arg Ser
 446 260 265 270
 449 Leu Lys Lys Tyr Tyr Gly His Gly Ala Gly Asn Pro Leu Gly Pro Thr
 450 275 280 285
 453 Gln Gly Val Gly Tyr Ala Asn Glu Leu Ile Ala Arg Leu Thr His Ser
 454 290 295 300
 457 Pro Val His Asp Asp Thr Ser Ser Asn His Thr Leu Asp Ser Asn Pro
 458 305 310 315 320
 461 Ala Thr Phe Pro Leu Asn Ser Thr Leu Tyr Ala Asp Phe Ser His Asp
 462 325 330 335
 465 Asn Gly Ile Ile Ser Ile Leu Phe Ala Leu Gly Leu Tyr Asn Gly Thr
 466 340 345 350
 469 Lys Pro Leu Ser Thr Thr Val Glu Asn Ile Thr Gln Thr Asp Gly
 470 355 360 365
 473 Phe Ser Ser Ala Trp Thr Val Pro Phe Ala Ser Arg Leu Tyr Val Glu

VERIFICATION SUMMARY

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